

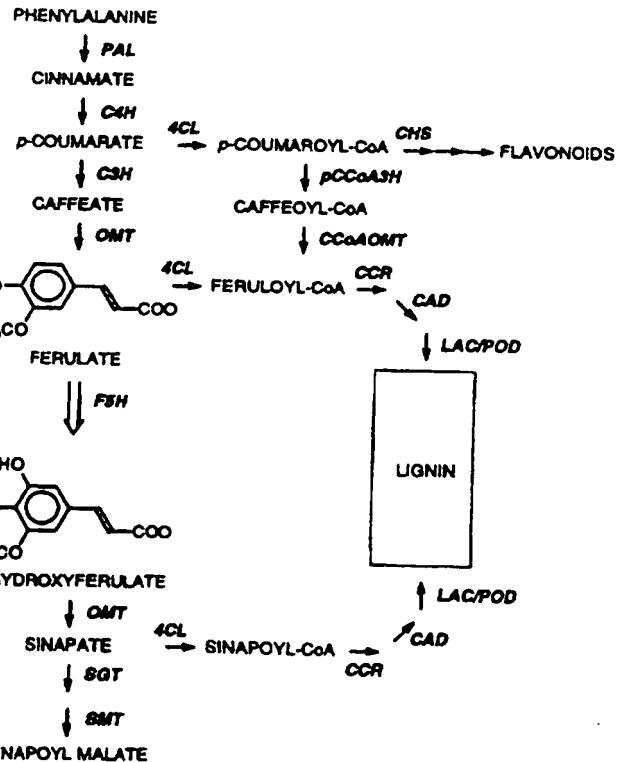
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(54) Title: A METHOD FOR REGULATION OF PLANT LIGNIN COMPOSITION

(57) Abstract

A method is disclosed for the regulation of lignin composition in plant tissue. Plants are transformed with a gene encoding an active F5H gene. The expression of the F5H gene results in increased levels of syringyl monomer providing a lignin composition more easily degraded with chemicals and enzymes.



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TITLEA METHOD FOR REGULATION OF PLANT LIGNIN COMPOSITION
FIELD OF INVENTION

The present method relates to the field of molecular biology and the regulation of protein synthesis through the introduction of foreign genes into plant genomes. More specifically, the method relates to the modification of plant lignin composition in a plant cell by the introduction of a foreign plant gene encoding an active ferulate-5-hydroxylase (F5H) enzyme. Plant transformants harboring the F5H gene demonstrate increased levels of syringyl monomer residues in their lignin, a trait that is thought to render the polymer more susceptible to delignification.

BACKGROUND

Lignin is one of the major products of the general phenylpropanoid pathway, and is one of the most abundant organic molecules in the biosphere (Crawford, (1981) *Lignin Biodegradation and Transformation*, New York: John Wiley and Sons). In nature, lignification provides rigidity to wood and is in large part responsible for the structural integrity of plant tracheary elements. Lignin is well suited to these capacities because of its physical characteristics and its resistance to biochemical degradation. Unfortunately, this same resistance to degradation has a significant impact on the utilization of lignocellulosic plant material (Whetten et al., *Forest Ecol. Management* 43, 301, (1991)).

The monomeric composition of lignin has significant effects on its chemical degradation during industrial pulping (Chiang et al., *Tappi*, 71, 173, (1988)). The guaiacyl lignins (derived from ferulic acid) characteristic of softwoods such as pine, require substantially more alkali and longer incubations during pulping in comparison to the guaiacyl-syringyl lignins (derived from ferulic acid and sinapic acid) found in hardwoods such as oak. The reasons for the differences between these two lignin types has been explored by measuring the degradation of model compounds such as guaiacylglycerol- β -guaiacyl ether, syringylglycerol- β -guaiacyl ether, and syringylglycerol- β -(4-methylsyringyl) ether (Kondo et al., *Holzforschung*, 41, 83, (1987)) under conditions that mimic those used in the pulping process. In these experiments, the mono- and especially di-syringyl compounds were cleaved three to fifteen times faster than their corresponding diguaiacyl homologues. These model studies are in agreement with studies comparing the pulping of Douglas fir and sweetgum wood where the major differences in the rate of pulping occurred above 150 °C where arylglycerol- β -aryl ether linkages were cleaved (Chiang et al., *Holzforschung*, 44, 309, (1990)).

Another factor affecting chemical degradation of the two lignin forms may be the condensation of lignin-derived guaiacyl and syringyl residues to form diphenylmethane units. The presence of syringyl residues in hardwood lignins leads to the formation of syringyl-containing diphenylmethane derivatives that

5 remain soluble during pulping, while the diphenylmethane units produced during softwood pulping are alkali-insoluble and thus remain associated with the cellulosic products (Chiang et al., *Holzforschung*, 44, 147, (1990); Chiang et al., *Holzforschung*, 44, 309, (1990)). Further, it is thought that the abundance of 5-5'-diaryl crosslinks that can occur between guaiacyl residues contributes to

10 resistance to chemical degradation. This linkage is resistant to alkali cleavage and is much less common in lignin that is rich in syringyl residues because of the presence of the 5-*O*-methyl group in syringyl residues. The incorporation of syringyl residues results in what is known as "non-condensed lignin", a material that is significantly easier to pulp than condensed lignin.

15 Similarly, lignin composition and content in grasses is a major factor in determining the digestibility of lignocellulosic materials that are fed to livestock (Jung, H.G. & Deetz, D.A. (1993) Cell wall lignification and degradability in Forage Cell Wall Structure and Digestibility (H.G. Jung, D.R. Buxton, R.D. Hatfield, and J. Ralph eds.), ASA/CSSA/SSSA Press, Madison, WI.). The

20 incorporation of the lignin polymer into the plant cell wall prevents microbial enzymes from having access to the cell wall polysaccharides that make up the wall. As a result, these polysaccharides cannot be degraded and much of the valuable carbohydrates contained within animal feedstocks pass through the animals undigested. Thus, an increase in the dry matter of grasses over the growing season

25 is counteracted by a decrease in digestibility caused principally by increased cell wall lignification. From these examples, it is clear that the modification of lignin monomer composition would be economically advantageous.

The problem to be overcome, therefore, is to develop a method for the creation of plants with increased levels of syringyl residues in their lignin to facilitate its chemical degradation. Modification of the enzyme pathway responsible for the production of lignin monomers provides one possible route to solving this problem.

The mechanism(s) by which plants control lignin monomer composition has been the subject of much speculation. As mentioned earlier, gymnosperms do not synthesize appreciable amounts of syringyl lignin. In angiosperms, syringyl lignin deposition is developmentally regulated: primary xylem contains guaiacyl lignin, while the lignin of secondary xylem and sclerenchyma is guaiacyl-syringyl lignin (Venverloo, *Holzforschung* 25, 18 (1971); Chapple et al., *Plant Cell* 4, 1413,

(1992)). No plants have been found to contain purely syringyl lignin. It is still not clear how this specificity is controlled; however, at least five possible enzymatic control sites exist, namely caffeic acid/5-hydroxyferulic acid *O*-methyltransferase (OMT), F5H, (hydroxy)cinnamoyl-CoA ligase (4CL), (hydroxy)cinnamoyl-CoA reductase (CCR), and (hydroxy)cinnamoyl alcohol dehydrogenase (CAD). For example, the substrate specificities of OMT (Shimada et al., *Phytochemistry*, 22, 2657, (1972); Shimada et al., *Phytochemistry*, 12, 2873, (1973); Gowri et al., *Plant Physiol.*, 97, 7, (1991); Bugos et al., *Plant Mol. Biol.* 17, 1203, (1992)) and CAD (Sarni et al., *Eur. J. Biochem.*, 139, 259, (1984); Goffner et al., *Planta*, 188, 48, (1992); O'Malley et al., *Plant Physiol.*, 98, 1364, (1992)) are correlated with the differences in lignin monomer composition seen in gymnosperms and angiosperms, and the expression of 4CL isozymes (Grand et al., *Physiol. Veg.* 17, 433, (1979); Grand et al., *Planta*, 158, 225, (1983)) has been suggested to be related to the tissue specificity of lignin monomer composition seen in angiosperms.

Although there are at least five possible enzyme targets that could be exploited, only OMT and CAD have been investigated in recent attempts to manipulate lignin monomer composition in transgenic plants (Dwivedi et al., *Plant Mol. Biol.* 26, 61, (1994); Halpin et al., *Plant J.* 6, 339, (1994); Ni et al., *Transgen. Res.* 3, 120 (1994); Atanassova et al., *Plant J.* 8, 465, (1995); Doorsselaere et al., *Plant J.* 8, 855, (1995)). Most of these studies have focused on sense and antisense suppression of OMT expression. This approach has met with variable results, probably owing to the degree of OMT suppression achieved in the various studies. The most dramatic effects were seen by using homologous OMT constructs to suppress OMT expression in tobacco (Atanassova et al., *supra*) and poplar (Doorsselaere et al., *supra*). Both of these studies found that as a result of transgene expression, there was a decrease in the content of syringyl lignin and a concomitant appearance of 5-hydroxyguaiacyl residues. As a result of these studies, Doorsselaere et al., (WO 9305160) disclose a method for the regulation of lignin biosynthesis through the genomic incorporation of an OMT gene in either the sense or anti-sense orientation. In contrast, Dixon et al. (WO 9423044) demonstrate the reduction of lignin content in plants transformed with an OMT gene, rather than a change in lignin monomer composition. Similar research has focused on the suppression of CAD expression. The conversion of coniferaldehyde and sinapaldehyde to their corresponding alcohols in transgenic tobacco plants has been modified with the incorporation of an *A. cordata* CAD gene in anti-sense orientation (Hibino et al., *Biosci. Biotechnol. Biochem.*, 59, 929, (1995)). A similar effort aimed at antisense inhibition of CAD expression

generated a lignin with increased aldehyde content, but only a modest change in lignin monomer composition (Halpin et al., *supra*). This research has resulted in the disclosure of methods for the reduction of CAD activity using sense and anti-sense expression of a cloned CAD gene to effect inhibition of endogenous CAD expression in tobacco [Boudet et al., (U.S. 5,451,514) and Walter et al., (WO 9324638); Bridges et al., (CA 2005597)]. None of these strategies increased the syringyl content of lignin, a trait that is correlated with improved digestibility and chemical degradability of lignocellulosic material (Chiang et al., *supra*; Chiang and Funaoka, *Holzforschung* 44, 309 (1990); Jung et al., *supra*).

10 Although F5H is also a key enzyme in the biosynthesis of syringyl lignin monomers it has not been exploited to date in efforts to engineer lignin quality. In fact, since the time of its discovery over 30 years ago (Higuchi et al., *Can. J. Biochem. Physiol.*, 41, 613, (1963)) there has been only one demonstration of the activity of F5H published (Grand, C., *FEBS Lett.* 169, 7, (1984)). Grand demonstrated that F5H from poplar was a cytochrome P450-dependent monooxygenase (P450) as analyzed by the classical criteria of dependence on NADPH and light-reversible inhibition by carbon monoxide. Grand further demonstrated that F5H is associated with the endoplasmic reticulum of the cell. The lack of attention given to F5H in recent years may be attributed in general to the difficulties associated with dealing with membrane-bound enzymes, and specifically to the lability of F5H when treated with the detergents necessary for solubilization (Grand, *supra*). The most recent discovery surrounding the F5H gene has been made by Chapple et al., (*supra*) who reported a mutant of *Arabidopsis thaliana* L. Heynh named *fah1* that is deficient in the accumulation of 20 sinapic acid-derived metabolites, including the guaiacyl-syringyl lignin typical of angiosperms. This locus, termed FAH1, encodes F5H. The cloning of the gene encoding F5H would provide the opportunity to test the hypothesis that F5H is a useful target for the engineering of lignin monomer composition.

25 In spite of sparse information about F5H in the published literature, Applicant has been successful in the isolation, cloning, and sequencing of the F5H gene. Applicant has also demonstrated that the stable integration of the F5H gene into the plant genome, where the expression of the F5H gene is under the control of a promoter other than the gene's endogenous promoter, leads to an altered regulation of lignin biosynthesis.

30 SUMMARY OF THE INVENTION

35 The present invention provides isolated nucleic-acid fragments comprising the nucleotide sequences which correspond to SEQ ID NO.:1 and SEQ ID NO.:3 encoding an active plant F5H enzyme wherein the enzyme has the amino acid

sequence encoded by the mature functional protein which corresponds to SEQ ID NO.:2 and wherein the amino acid sequence encompasses amino acid substitutions, additions and deletions that do not alter the function of the F5H enzyme.

5 The invention further provides a chimeric gene causing altered guaiacyl:syringyl lignin monomer ratios in a transformed plant, the gene comprising a nucleic acid fragment encoding an active plant F5H enzyme operably linked in either sense or antisense orientation to suitable regulatory sequences. The nucleic acid fragments are those described above.

10 Also provided is a method of altering the activity of F5H in a plant by means of transforming plant cells in a whole plant with a chimeric gene causing altered guaiacyl:syringyl lignin monomer ratios in a transformed plant cell, wherein the gene is expressed; growing said plants under conditions that permit seed development; and screening the plants derived from these transformed seeds for those that express an active F5H gene or fragment thereof.

15 A method is provided of altering the activity of F5H enzyme in a plant by (i) transforming a cell, tissue or organ from a suitable host plant with the chimeric gene described above wherein the chimeric gene is expressed; (ii) selecting transformed cells, cell callus, somatic embryos, or seeds which contain the chimeric gene; (iii) regenerating whole plants from the transformed cells, cell callus, somatic embryos, or seeds selected in step (ii); (iv) selecting whole plants regenerated in step (iii) which have a phenotype characterized by (1) an ability of the whole plant 20 to accumulate compounds derived from sinapic acid or (2) an altered syringyl lignin monomer content relative to an untransformed host plant.

25 The invention additionally provides a method of altering the composition of lignin in a plant by means of stably incorporating into the genome of the host plant by transformation a chimeric gene causing altered guaiacyl:syringyl lignin monomer ratios in a transformed plant; expressing the incorporated gene such that F5H is expressed and wherein guaiacyl:syringyl lignin monomer ratios are altered from those ratios of the untransformed host plant.

30 **BRIEF DESCRIPTION OF THE FIGURES AND SEQUENCE LISTING**

Figure 1 illustrates the biosynthesis of monomeric lignin precursors via the general phenylpropanoid pathway.

35 Figure 2 is an illustration of the pBIC20-F5H cosmid and the F5H overexpression construct (pGA482-35S-F5H) in which the F5H gene is expressed under the control of the constitutive cauliflower mosaic virus 35S promoter.

Figure 3 shows an analysis of sinapic acid-derived secondary metabolites in wild type, the *fahl-2* mutant, and independently-derived transgenic *fahl-2* plants

carrying the T-DNA derived from the pBIC20-F5H cosmid, or the pGA482-35S-F5H overexpression construct.

Figure 4 shows the impact of F5H overexpression by comparing the steady state levels of F5H mRNA in wild type, the *fahl-2* mutant, and independently-derived transgenic *fahl-2* plants carrying the T-DNA derived from the 35S-F5H overexpression construct.

Figure 5 shows a GC analysis of lignin nitrobenzene oxidation products to illustrate the impact of F5H overexpression on lignin monomer composition in the wild type, the *fahl-2* mutant, and a *fahl-2* mutant carrying the T-DNA derived from the 35S-F5H overexpression construct.

Figure 6 illustrates a Southern blot analysis comparing hybridization of the F5H cDNA to *Eco*RI digested genomic DNA isolated from wild type *Arabidopsis thaliana* and a number of *fahl* mutants.

Figure 7 is a Northern blot analysis comparing hybridization of the F5H cDNA to RNA isolated from wild type *Arabidopsis thaliana* and a number of *fahl* mutants.

Figure 8 shows the genomic nucleotide (SEQ ID NO.:3) and amino acid (SEQ ID NO.:2) sequences of the *Arabidopsis* F5H gene and the F5H enzyme that it encodes.

Applicant(s) have provided three sequence listings in conformity with 37 C.F.R. 1.821-1.825 and Appendices A and B ("Requirements for Application Disclosures Containing Nucleotides and/or Amino Acid Sequences") and in conformity with "Rules for the Standard Representation of Nucleotide and Amino Acid Sequences in Patent Applications" and Annexes I and II to the Decision of the President of the EPO, published in Supplement No 2. to OJ EPO, 12/1992.

The sequence of the *Arabidopsis thaliana* F5H cDNA is given in SEQ ID NO.:1 and the sequence of the *Arabidopsis thaliana* F5H genomic clone is given in SEQ ID NO.:3. The sequence of the F5H protein is given in SEQ ID NO.:2.

DETAILED DESCRIPTION OF THE INVENTION

The present invention provides a gene that encodes F5H, a key enzyme in lignin biosynthesis. The invention further provides a method for altering the lignin composition in plants by transforming plants with the F5H gene wherein the gene is expressed and causes an increased conversion of ferulic acid to sinapic acid thereby increasing the syringyl content of the lignin polymer.

The effect in plants of lignin compositions containing higher syringyl monomer content is that the lignin is more susceptible to chemical delignification. This is of particular use in the paper and pulp industries where vast amounts of energy and time are consumed in the delignification process. Woody plants

transformed with an active F5H gene would offer a significant advantage in the delignification process over conventional paper feedstocks. Similarly, modification of the lignin composition in grasses by the insertion and expression of a heterologous F5H gene offers a unique method for increasing the digestibility of 5 livestock feed. Maximizing the digestibility of grasses in this manner offers great potential economic benefit to the farm and agricultural industries.

Plants to which the Invention may be Applied

The invention provides a gene and a chimeric gene construct useful for the transformation of plant tissue for the alteration of lignin monomer composition.

10 Plants suitable in the present invention comprise plants that naturally lack syringyl lignin or those that accumulate lignin with a high guaiacyl:syringyl ratio. Plants suitable in the present invention also comprise plants whose lignin could be modified using antisense transformation constructs that reduce the syringyl content of the transgenic plants' lignin if such an alteration were desirable.

15 Suitable plants may include but are not limited to alfalfa (*Medicago* sp.), rice (*Oryza* sp.), maize (*Zea mays*), oil seed rape (*Brassica* sp.), forage grasses, and also tree crops such as eucalyptus (*Eucalyptus* sp.), pine (*Pinus* sp.), spruce (*Picea* sp.) and poplar (*Populus* sp.), as well as *Arabidopsis* sp. and tobacco (*Nicotiana* sp.).

20 **Definitions**

As used herein the following terms may be used for interpretation of the claims and specification.

The term "FAH1" refers to the locus or chromosomal location at which the F5H gene is encoded. The term "FAH1" refers to the wild type allele of the gene 25 encoding the F5H gene. The term "fahl" refers to any mutant version of that gene that leads to an altered level of enzyme activity, syringyl lignin content or sinapate ester content that can be measured by thin layer chromatography, high performance liquid chromatography, or by *in vivo* fluorescence.

"Gene" refers to a nucleic acid fragment that expresses a specific protein, 30 including regulatory sequences preceding (5' non-coding) and following (3' non-coding) the coding region. "Native" gene refers to the gene as found in nature with its own regulatory sequences.

A "chimeric gene" refers to a gene comprising heterogeneous regulatory and coding sequences.

35 An "endogenous gene" refers to the native gene normally found in its natural location in the genome.

A "foreign gene" or "transgene" refers to a gene not normally found in the host organism but one that is introduced by gene transfer.

The term "promoter" refers to a DNA sequence in a gene, usually upstream (5') to its coding sequence, which controls the expression of the coding sequence by providing the recognition site for RNA polymerase and other factors required for proper transcription. A promoter may also contain DNA sequences that are 5 involved in the binding of protein factors which control the effectiveness of transcription initiation in response to physiological or developmental conditions.

The term "operably linked" refers to nucleic acid sequences on a single nucleic acid molecule which are associated so that the function of one is affected by the other.

10 As used herein, suitable "regulatory sequences" refer to nucleotide sequences located upstream (5'), within, and/or downstream (3') of a coding sequence, which control the transcription and/or expression of the coding sequences in conjunction with the protein biosynthetic apparatus of the cell. These regulatory sequences include promoters, translation leader sequences, transcription 15 termination sequences, and polyadenylation sequences.

The term "T-DNA" refers to the DNA that is transferred into the plant genome from a T-DNA plasmid carried by a strain of *Agrobacterium tumefaciens* that is used to infect plants for the purposes of plant transformation.

20 The term "T-DNA plasmid" refers to a plasmid carried by *Agrobacterium tumefaciens* that carries an origin of replication, selectable markers such as antibiotic resistance, and DNA sequences referred to as right and left borders that are required for plant transformation. The DNA sequence that is transferred during this process is that which is located between the right and left T-DNA 25 border sequences present on a T-DNA plasmid. The DNA between these borders can be manipulated in such a way that any desired sequence can be inserted into the plant genome.

30 The term "ferulate-5-hydroxylase" or "F5H" will refer to an enzyme in the plant phenylpropanoid biosynthetic pathway which catalyzes the conversion of ferulate to 5-hydroxyferulate and permits the production of sinapic acid and its subsequent metabolites, including sinapoylmalate and syringyl lignin.

The terms "encoding" and "coding" refer to the process by which a gene, through the mechanisms of transcription and translation, provides the information to a cell from which a series of amino acids can be assembled into a specific amino acid sequence to produce an active enzyme. It is understood that the process of 35 encoding a specific amino acid sequence includes DNA sequences that may involve base changes that do not cause a change in the encoded amino acid, or which involve base changes which may alter one or more amino acids, but do not affect the functional properties of the protein encoded by the DNA sequence. It is

therefore understood that the invention encompasses more than the specific exemplary sequences. Modifications to the sequence, such as deletions, insertions, or substitutions in the sequence which produce silent changes that do not substantially affect the functional properties of the resulting protein molecule are 5 also contemplated. For example, alterations in the gene sequence which reflect the degeneracy of the genetic code, or which result in the production of a chemically equivalent amino acid at a given site, are contemplated. Thus, a codon for the amino acid alanine, a hydrophobic amino acid, may be substituted by a codon encoding another less hydrophobic residue, such as glycine, or a more hydrophobic 10 residue, such as valine, leucine, or isoleucine. Similarly, changes which result in substitution of one negatively charged residue for another, such as aspartic acid for glutamic acid, or one positively charged residue for another, such as lysine for arginine, can also be expected to produce a biologically equivalent product. Nucleotide changes which result in alteration of the N-terminal and C-terminal 15 portions of the protein molecule would also not be expected to alter the activity of the protein. In some cases, it may in fact be desirable to make mutants of the sequence in order to study the effect of alteration on the biological activity of the protein. Each of the proposed modifications is well within the routine skill in the art, as is determination of retention of biological activity in the encoded products. 20 Moreover, the skilled artisan recognizes that sequences encompassed by this invention are also defined by their ability to hybridize, under stringent conditions (2X SSC, 0.1% SDS, 65 °C), with the sequences exemplified herein.

The term "expression", as used herein, refers to the production of the protein product encoded by a gene. "Overexpression" refers to the production of a 25 gene product in transgenic organisms that exceeds levels of production in normal or non-transformed organisms.

"Transformation" refers to the transfer of a foreign gene into the genome of a host organism and its genetically stable inheritance. Examples of methods of plant transformation include *Agrobacterium*-mediated transformation and particle-accelerated or "gene gun" transformation technology as described in 30 U.S. 5,204,253.

The term "plasmid rescue" will refer to a technique for circularizing restriction enzyme-digested plant genomic DNA that carries T-DNA fragments bearing a bacterial origin of replication and antibiotic resistance (encoded by the 35 β-lactamase gene of *E. coli*) such that this circularized fragment can be propagated as a plasmid in a bacterial host cell such as *E. coli*.

The term "lignin monomer composition" refers to the relative ratios of guaiacyl monomer and syringyl monomer found in lignified plant tissue.

The Phenylpropanoid Biosynthetic Pathway

The lignin biosynthetic pathway is well researched and the principal pathways are illustrated in Figure 1. Lignin biosynthesis is initiated by the conversion of phenylalanine into cinnamate through the action of phenylalanine ammonia lyase (PAL). The second enzyme of the pathway is cinnamate-4-hydroxylase (C4H), a cytochrome P450-dependent monooxygenase (P450) which is responsible for the conversion of cinnamate to *p*-coumarate. The second hydroxylation of the pathway is catalyzed by a relatively ill-characterized enzyme, *p*-coumarate-3-hydroxylase (C3H), whose product is caffeic acid. Caffeic acid is subsequently *O*-methylated by OMT to form ferulic acid, a direct precursor of lignin. The last hydroxylation reaction of the general phenylpropanoid pathway is catalyzed by F5H. The 5-hydroxyferulate produced by F5H is then *O*-methylated by OMT, the same enzyme that carries out the *O*-methylation of caffeic acid. This dual specificity of OMT has been confirmed by the cloning of the OMT gene, and expression of the protein in *E. coli* (Bugos et al., (1991) *supra*; Gowri et al., (1991) *supra*).

The committed steps of lignin biosynthesis are catalyzed by 4CL, (hydroxy)cinnamoyl CoA reductase (CCR) and CAD, which ultimately generate coniferyl alcohol from ferulic acid and sinapoyl alcohol from sinapic acid. Coniferyl alcohol and sinapoyl alcohol are polymerized by extracellular oxidases to yield guaiacyl lignin and syringyl lignin respectively, although syringyl lignin is more accurately described as a co-polymer of both monomers.

Although ferulic acid, sinapic acid, and in some cases *p*-coumaric acid are channeled into lignin biosynthesis, in some plants these compounds are precursors for other secondary metabolites. In *Arabidopsis*, sinapic acid serves as a precursor for lignin biosynthesis but it is also channeled into the synthesis of soluble sinapic acid esters. In this pathway, sinapic acid is converted to sinapoylglucose which serves as an intermediate in the biosynthesis of sinapoylmalate (Figure 5). Sinapic acid and its esters are fluorescent and may be used as a marker of plants deficient in those enzymes needed to produce sinapic acid (Chapple et al., *supra*).

Identification of the FAH1 Locus and *fah1* Alleles

A series of mutants of *Arabidopsis* that fail to accumulate sinapoylmalate have been identified and have been collectively termed *fah1* mutants. The fluorescent nature of sinapoylmalate permits the facile identification of sinapic acid esters by thin layer chromatography (TLC) followed by observation under ultraviolet (UV) light. The fluorescence of sinapoylmalate can also be visualized *in vivo* because sinapoylmalate is accumulated in the adaxial leaf epidermis. Wild type *Arabidopsis* exhibits a pale blue fluorescence under UV while *fah1* mutants

appear dark red because of the lack of the blue fluorescence of sinapoylmalate and the fluorescence of chlorophyll in the subtending mesophyll (Chapple et al., *supra*).

A TLC-based mutant screen of 4,200 ethyl methanesulfonate-mutagenized *Arabidopsis* plants identified a number of independent mutant lines that 5 accumulated significantly lower levels of sinapoylmalate. The mutations in these lines were identified as *fah1-1* through *fah1-5*. The *in vivo* UV-fluorescence visual screen was used to identify more mutant lines carrying the *fah1* mutation. Two of these mutants (*fah1-6* and *fah1-7*) were selected from EMS-mutagenized 10 populations. One mutant line (*fah1-8*) was selected from among a mutant population generated by fast-neutron bombardment (Nilan, R. A. *Nucl. Sci. Abstr.*, 28(3), 5940 (1973); Kozer et al., *Genet. Pol.*, 26(3), 367, (1985)). A final mutant line, (*fah1-9*) was identified using the same technique from a T-DNA tagged 15 population of plants. Before further analysis, each mutant line was backcrossed at least twice to the wild type and homozygous lines were established.

15 To determine whether the newly isolated mutant lines were defective at the same locus, that is, within the gene encoding F5H, genetic complementation experiments were performed. In these tests, each mutant line was crossed to *fah1-2* which is known to be defective in F5H. In each case, the newly isolated 20 mutant line was used as the female parent and was fertilized with pollen from a *fah1-2* homozygous mutant. A reciprocal cross was also performed using *fah1-2* as the female parent, and the new mutant line as the pollen donor. The seeds from 25 these crosses were collected several weeks later, and were planted for subsequent analysis. The progeny were analyzed for sinapoylmalate production by TLC, high pressure liquid chromatography and by observation under UV light. From these crosses, all of the F1 progeny examined were sinapoylmalate-deficient, indicating that all of the mutations identified were allelic.

30 The *fah1-9* line was selected for further study because of the presence of the T-DNA insertion within the F5H gene. The T-DNA insertion within the FAH1 locus facilitated the cloning of the flanking *Arabidopsis* DNA which could then be used to retrieve the wild type F5H gene from cDNA and genomic libraries (Meyer et al., *Proc. Natl. Acad. Sci. USA*, 93, 6869 (1996)).

Cloning of the FAH1 Locus

35 A fragment of DNA from the FAH1 locus was isolated from the T-DNA tagged *fah1-9* mutant using the technique of plasmid rescue (Meyer et al., *supra*). The technique of plasmid rescue is common and well known in the art and may be used to isolate specific alleles from T-DNA transformed plants (Behringer, et al., *Plant Mol. Biol. Rep.*, 10, 190,(1992)). Briefly, the vector used to generate the T-DNA tagged population of *Arabidopsis* carries sequences required for

autonomous replication of DNA in bacteria and sequences that confer antibiotic resistance. Once this DNA is integrated into the plant genome, specific restriction endonuclease digests can be employed to generate fragments that can be circularized, ligated, and transformed into *E. coli*. Circularized DNA from the 5 T-DNA will generate functional plasmids that confer antibiotic resistance to their bacterial hosts such that they can be identified by growth on selective media. Those plasmids that are generated from the sequences including the right and left borders will also carry with them the plant genomic sequences flanking the T-DNA insertion. Plasmids generated from either of the T-DNA borders that carry 10 flanking DNA sequences can be identified by analyzing the products of diagnostic restriction enzyme digests on agarose gels. The plasmids with flanking sequences can then serve as a starting point for cloning plant sequences that share homology to the DNA at the point of T-DNA insertion (Behringer, et al., *supra*).

Plasmid rescue was conducted using *Eco*RI-digested DNA prepared from 15 homozygous *fahl-9* plants. *Eco*RI-digested genomic DNA was ligated and then electroporated into competent DH5 α *E. coli*. DNA from rescued plasmids was further digested with both *Eco*RI and *Sal*I and the digests were analyzed by gel electrophoresis to identify plasmids that contained flanking *Arabidopsis* DNA. A 20 *Sac*II-*Eco*RI fragment from this rescued plasmid was used to identify an F5H clone from an *Arabidopsis* cDNA library (Newman, T. et al., *Plant. Physiol.* 106, 1241, (1994)).

DNA Sequencing of the F5H cDNA and genomic clones

Sequence analysis of the F5H cDNA and genomic clones was performed on 25 plasmid DNA manually using a United States Biochemical Sequenase Kit v. 2.0, on a DuPont Genesis[®] 2000 sequencer or on an Applied Biosystems 373A DNA sequencer, using standard vector-based sequencing oligonucleotides or custom-synthesized oligonucleotides as appropriate. The sequence of the *Arabidopsis thaliana* F5H cDNA is given in SEQ ID NO.:1 and the sequence of the *Arabidopsis thaliana* F5H genomic clone is given in SEQ ID NO.:3.

30 The F5H cDNA contains a 1560 bp open reading frame that encodes a protein with a molecular weight of 58,728. The putative ATG initiation codon is flanked by an A at -3 and a G at +4, in keeping with the nucleotides commonly found flanking the initiator methionine in plant mRNAs (Lutcke et al., *EMBO J.* 6, 43, (1987)). Immediately following the inferred initiator methionine is a 17 amino 35 acid sequence containing nine hydroxy amino acids (Figure 8). The subsequent fifteen amino acid sequence is rich in hydrophobic amino acids; eleven hydrophobic residues comprised of phenylalanine, isoleucine, leucine and valine residues. This hydrophobic stretch is immediately followed by an Arg-Arg-Arg-Arg putative stop

transfer sequence. F5H also shares significant sequence identity with other P450s. Most notable is the stretch between Pro-450 and Gly-460. This region contains eight residues that comprise the heme-binding domain and are highly conserved among most P450s, one exception being allene oxide synthase from *Linum usitatissimum* (Song et al., *Proc. Natl. Acad. Sci. USA* 90, 8519, (1993)). The Pro-450 to Gly-460 region contains Cys-458 in F5H, which by analogy is most likely the heme binding ligand in this enzyme.

5 Transformation of *fah1-2* *Arabidopsis* and Restoration of Sinapoylmalate Accumulation

10 The identity of the F5H gene was confirmed by complementation of the *fah1-2* mutant with a genomic clone and a construct where the F5H genomic coding sequence was expressed under the control of the cauliflower mosaic virus 35S promoter. Briefly, the F5H cDNA was used as a probe to screen a transformation competent library (Meyer et al., (1994) *Science*, 264, 1452-1455) for genomic clones. Using this method, a cosmid clone (pBIC20-F5H) was isolated that carried a 17kb genomic insert containing the inferred start and stop codons of the F5H gene (Figure 2). The portion of this cosmid carrying the F5H open reading frame was excised from the cosmid and subcloned into a vector in which it was operably linked to the cauliflower mosaic virus 35S promoter

15 (pGA482-35S-F5H) (Figure 2). Both the original cosmid and this derivative plasmid construct were electroporated into *Agrobacterium tumefaciens* and were used to transform *fah1-2* mutants. Success of the transformations was evidenced by TLC assays demonstrating sinapoylmalate accumulation in leaf tissues of the *fah1-2* transformants carrying the T-DNA from the pBIC20-F5H cosmid or the

20 pGA482-35S-F5H plasmid (Figure 3). These data clearly indicated that the gene encoding F5H had been identified.

25

Modification of Lignin Composition in Plants Transformed With F5H Under the Control of the Cauliflower Mosaic Virus 35S Promoter

Arabidopsis plants homozygous for the *fah1-2* allele were transformed with *Agrobacterium* carrying the pGA482-35S-F5H plasmid which contains the chimeric F5H gene under the control of the constitutive cauliflower mosaic virus 35S promoter (Odell, et al., *Nature* 313, 810-812, (1985)). Independent homozygous transformants carrying the F5H transgene at a single genetic locus were identified by selection on kanamycin-containing growth media, grown up in soil and plant tissue was analyzed for lignin monomer composition. Nitrobenzene oxidation analysis of the lignin in wild type, *fah1-2*, and transformants carrying the T-DNA from the pGA482-35S-F5H construct revealed that F5H overexpression as measured by northern blot analysis (Figure 4) led to a significant increase in

syringyl content of the transgenic lignin (Figure 5). The lignin of the F5H-overexpressing plants demonstrated a syringyl content as high as 29 mol% as opposed to the syringyl content of the wild type lignin which was 18 mol% (Table 1) (Example 5). These data clearly demonstrate that overexpression of the 5 F5H gene is useful for the alteration of lignin composition in transgenic plants.

TABLE 1
Impact of 35S Promoter-Driven F5H Expression on
Lignin Monomer Composition in *Arabidopsis*

Line	Total G units ^a ($\mu\text{mol g}^{-1}$ d.w.)	Total S units ^b ($\mu\text{mol g}^{-1}$ d.w.)	Total G+S units ($\mu\text{mol g}^{-1}$ d.w.)	mol % S
wild type	3.33 +/- 0.32	0.75 +/- 0.09	4.09 +/- 0.41	18.4 +/- 0.91
<i>fah1-2</i>	5.44 +/- 0.45	n.d.	5.44 +/- 0.45	-
88	6.63 +/- 0.75	0.35 +/- 0.04	6.99 +/- 0.79	5.06 +/- 0.17
172	4.21 +/- 0.36	0.67 +/- 0.07	4.88 +/- 0.42	13.7 +/- 0.55
170	4.08 +/- 0.33	0.97 +/- 0.06	5.05 +/- 0.37	19.2 +/- 0.56
122	3.74 +/- 0.20	0.93 +/- 0.05	4.66 +/- 0.22	19.9 +/- 0.86
108	5.40 +/- 0.48	1.59 +/- 0.18	6.98 +/- 0.65	22.7 +/- 0.82
107	5.74 +/- 0.60	1.96 +/- 0.31	7.70 +/- 0.89	25.3 +/- 1.23
180	3.85 +/- 0.31	1.34 +/- 0.11	5.19 +/- 0.40	25.8 +/- 0.78
117	3.21 +/- 0.30	1.18 +/- 0.13	4.39 +/- 0.43	28.8 +/- 0.92
128	3.46 +/- 0.22	1.39 +/- 0.17	5.05 +/- 0.37	27.5 +/- 1.80

^asum of vanillin + vanillic acid

^bsum of syringaldehyde + syringic acid

In a similar fashion, T1 tobacco (*Nicotiana tabacum*) F5H transformants were generated, grown up and analyzed for lignin monomer composition.

10 Nitrobenzene oxidation analysis demonstrated that the syringyl monomer content of the leaf midribs was increased from 14 mol% in the wild type to 40 mol% in the transgenic line that most highly expressed the F5H transgene (Table 2).

TABLE 2
Impact of 35S Promoter-Driven F5H Expression on Lignin Monomer
Composition in Tobacco Leaf Midrib Xylem

Line	Total G units ^a ($\mu\text{mol g}^{-1}$ d.w.)	Total S units ^b ($\mu\text{mol g}^{-1}$ d.w.)	Total G+S units ($\mu\text{mol g}^{-1}$ d.w.)	mol % S
wild type	1.40 +/- 0.26	0.23 +/- 0.04	1.63 +/- 0.30	14.3 +/- 1.09
40	0.86 +/- 0.16	0.24 +/- 0.03	1.11 +/- 0.20	22.4 +/- 1.53
27	1.13 +/- 0.11	0.52 +/- 0.05	1.65 +/- 0.16	31.3 +/- 0.50
48	1.28 +/- 0.32	0.71 +/- 0.19	1.99 +/- 0.43	35.7 +/- 6.06
33	0.65 +/- 0.17	0.43 +/- 0.11	1.09 +/- 0.27	40.0 +/- 1.86

^asum of vanillin + vanillic acid

^bsum of syringaldehyde + syringic acid

Construction of Chimeric Genes for the Expression of F5H in Plants.

The expression of foreign genes in plants is well-established (De Blaere et al. (1987) *Meth. Enzymol.* 143:277-291) and this invention provides for a method 5 to apply this technology to the introduction of a chimeric gene for the overexpression of the F5H gene in plants for the manipulation of lignin monomer composition. The expression of the F5H mRNAs at an appropriate level may require the use of different chimeric genes utilizing different promoters. A preferred class of heterologous hosts for the expression of the coding sequence of 10 the F5H gene are eukaryotic hosts, particularly the cells of higher plants. Particularly preferred among the higher plants and the seeds derived from them are alfalfa (*Medicago* sp.), rice (*Oryza* sp.), maize (*Zea mays*), oil seed rape (*Brassica* sp.), forage grasses, and also tree crops such as eucalyptus (*Eucalyptus* sp.), pine (*Pinus* sp.), spruce (*Picea* sp.) and poplar (*Populus* sp.), as well as *Arabidopsis* sp. 15 and tobacco (*Nicotiana* sp.). Expression in plants will use regulatory sequences functional in such plants.

The origin of the promoter chosen to drive the expression of the coding sequence is not critical as long as it has sufficient transcriptional activity to accomplish the invention by expressing translatable mRNA for the F5H gene in the 20 desired host tissue. Preferred promoters will effectively target F5H expression to those tissues that undergo lignification. These promoters may include, but are not limited to promoters of genes encoding enzymes of the phenylpropanoid pathway such as the PAL promoter (Ohl et al., *Plant Cell*, 2, 837, (1990) and the 4CL promoter(Hauffed et al., *Plant Cell*, 3, 435, (1991).

25 Depending upon the application, it may be desirable to select promoters that are specific for expression in one or more organs of the plant. Examples include the light-inducible promoters of the small subunit of ribulose 1,5-bisphosphate carboxylase, if the expression is desired in photosynthetic organs, or promoters active specifically in roots.

30 Expression of F5H Chimeric Genes in Plants

Various methods of introducing a DNA sequence (i.e., of transforming) 35 into eukaryotic cells of higher plants are available to those skilled in the art (see EPO publications 0 295 959 A2 and 0 138 341 A1). Such methods include those based on transformation vectors based on the Ti and Ri plasmids of *Agrobacterium spp.* It is particularly preferred to use the binary type of these vectors. Ti-derived vectors transform a wide variety of higher plants, including monocotyledonous and dicotyledonous plants, such as soybean, cotton, tobacco, *Arabidopsis* and rape (Pacciotti et al., *Bio/Technology* 3, 241, (1985); Byrne et al., *Plant Cell, Tissue and Organ Culture* 8, 3, (1987); Sukhapinda et al., *Plant Mol. Biol.* 8, 209,

(1987); Lorz et al., *Mol. Gen. Genet.* 199, 178, (1985); Potrykus *Mol. Gen. Genet.* 199, 183, (1985)).

For introduction into plants the chimeric genes of the invention can be inserted into binary vectors as described in Example 5.

5 Other transformation methods are available to those skilled in the art, such as direct uptake of foreign DNA constructs [see EPO publication 0 295 959 A2], techniques of electroporation [see Fromm et al. (1986) *Nature* (London) 319:791] or high-velocity ballistic bombardment with metal particles coated with the nucleic acid constructs (see Kline et al., *Nature* (London) 327:70 (1987), and see U.S. 10 Patent No. 4,945,050). Once transformed, the cells can be regenerated by those skilled in the art.

The following Examples are meant to illustrate key embodiments of the invention but should not be construed to be limiting in any way.

EXAMPLES

15 GENERAL METHODS

Restriction enzyme digestions, phosphorylations, ligations and transformations were done as described in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Second Edition (1989) Cold Spring Harbor Laboratory Press. All reagents and materials used for the growth and maintenance of bacterial cells 20 were obtained from Aldrich Chemicals (Milwaukee, WI), DIFCO Laboratories (Detroit, MI), GIBCO/BRL (Gaithersburg, MD), or Sigma Chemical Company (St. Louis, MO) unless otherwise specified.

25 The meaning of abbreviations is as follows: "h" means hour(s), "min" means minute(s), "sec" means second(s), "d" means day(s), " μ L" means microliter(s), "mL" means milliliters, "L" means liters, "g" means grams, "mg" means milligrams, " μ g" means microgram(s), "nm" means nanometer(s), "m" means meter(s), "E" means Einstein(s).

Plant material

30 *Arabidopsis thaliana* was grown under a 16 h light/8 h dark photoperiod at 100 mE $m^{-2} s^{-1}$ at 24 °C cultivated in Metromix 2000 potting mixture (Scotts, Marysville OH). Mutant lines *fahl-1* through *fahl-5* were identified by TLC as described below. Using their red fluorescence under UV light as a marker, mutant lines *fahl-6*, *fahl-7*, and *fahl-8* were selected from ethylmethane sulfonate (*fahl-6*, *fahl-7*) or fast-neutron (*fahl-8*) mutagenized populations of Landsberg *erecta* M2 35 seed. The T-DNA tagged line 3590 (*fahl-9*) was similarly identified in the DuPont T-DNA tagged population (Feldmann, K.A., Malmberg, R.L., & Dean, C., (1994) *Mutagenesis in Arabidopsis in Arabidopsis*, (E. M. Meyerowitz and C. R. Somerville, eds.) Cold Spring Harbor Press). All lines were backcrossed to wild

type at least twice prior to experimental use to remove unlinked background mutations.

Secondary Metabolite Analysis

Leaf extracts were prepared from 100 mg samples of fresh leaf tissue suspended in 1 mL of 50% methanol. Samples were vortexed briefly, then frozen at -70 °C. Samples were thawed, vortexed, and centrifuged at 12,000 xg for 5 min. Sinapoylmalate content was qualitatively determined following silica gel TLC, in a mobile phase of n-butanol/ethanol/water (4:1:1). Sinapic acid and its esters were visualized under long wave UV light (365 nm) by their characteristic fluorescence.

Southern Analysis

For Southern analysis, DNA was extracted from leaf material (Rogers, et al., (1985) *Plant. Mol. Biol.* 5, 69), digested with restriction endonucleases and transferred to Hybond N+ membrane (Amersham, Cleveland Ohio) by standard protocols. cDNA probes were radiolabelled with ^{32}P and hybridized to the target membrane in Denhardt's hybridization buffer (900 mM sodium chloride, 6 mM disodium EDTA, 60 mM sodium phosphate pH 7.4, 0.5% SDS, 0.01% denatured herring sperm DNA and 0.1% each polyvinylpyrrolidone, bovine serum albumin, and Ficoll 400) containing 50% formamide at 42 °C. To remove unbound probe, membranes were washed twice at room temperature and twice at 65 °C in 2x SSPE (300 mM sodium chloride, 2 mM disodium EDTA, 20 mM sodium phosphate, pH 7.4) containing 0.1% SDS, and exposed to film.

Northern Analysis

RNA was first extracted from leaf material according to the following protocol.

For extraction of RNA, Covey's extraction buffer was prepared by dissolving 1% (w/v) TIPS (triisopropyl-naphthalene sulfonate, sodium salt), 6% (w/v) PAS (*p*-aminosalicylate, sodium salt) in 50 mM Tris pH 8.4 containing 5% v/v Kirby's phenol. Kirby's phenol was prepared by neutralizing liquified phenol containing 0.1% (w/v) 8-hydroxyquinoline with 0.1 M Tris-HCl pH 8.8. For each RNA preparation, a 1 g samples of plant tissue was ground in liquid nitrogen and extracted in 5 mL Covey's extraction buffer containing 10 μL β -mercaptoethanol. The sample was extracted with 5 mL of a 1:1 mixture of Kirby's phenol and chloroform, vortexed, and centrifuged for 20 min at 7,000 xg. The supernatant was removed and the nucleic acids were precipitated with 500 μL of 3 M sodium acetate and 5 mL isopropanol and collected by centrifugation at 10,000 xg for 10 min. The pellet was redissolved in 500 μL water, and the RNA was precipitated on ice with 250 μL 8 M LiCl, and collected by centrifugation at

10,000 xg for 10 min. The pellet was resuspended in 200 μ L water and extracted with an equal volume of chloroform:isoamyl alcohol 1:1 with vortexing. After centrifugation for 2 min at 10,000 xg, the upper aqueous phase was removed, and the nucleic acids were precipitated at -20 °C by the addition of 20 μ L 3 M sodium 5 acetate and 200 μ L isopropanol. The pellet was washed with 1 mL cold 70% ethanol, dried, and resuspended in 100 μ L water. RNA content was assayed spectrophotometrically at 260 nm. Samples containing 1 to 10 μ g of RNA were subjected to denaturing gel electrophoresis as described elsewhere (Sambrook et al., *supra*).

10 Extracted RNA was transferred to Hybond N⁺ membrane (Amersham, Cleveland Ohio), and probed with radiolabelled probes prepared from cDNA clones. Blots were hybridized overnight, washed twice at room temperature and once at 65 °C in 3x SSC (450 mM sodium chloride, 45 mM sodium citrate, pH 7.0) containing 0.1% SDS, and exposed to film.

15 Identification of cDNA and Genomic Clones

cDNA and genomic clones for F5H were identified by standard techniques using a 2.3 kb *Sac*II/*Eco*RI fragment from the rescued plasmid (pCC1) (Example 2) as a probe. The cDNA clone pCC30 was identified in the λ PRL2 library (Newman et al., (1994) *supra*) kindly provided by Dr. Thomas Newman 20 (DOE Plant Research Laboratory, Michigan State University, East Lansing, MI). A genomic cosmid library of *Arabidopsis thaliana* (ecotype Landsberg *erecta*) generated in the binary cosmid vector pBIC20 (Example 3) (Meyer et al., *Science* 264, 1452, (1994)) was screened with the radiolabelled cDNA insert derived from pCC30. Genomic inserts in the pBIC20 T-DNA are flanked by the neomycin 25 phosphotransferase gene for kanamycin selection adjacent to the T-DNA right border sequence, and the β -glucuronidase gene for histochemical selection adjacent to the left border. Positive clones were characterized by restriction digestion and Southern analysis in comparison to *Arabidopsis* genomic DNA.

Plant transformation

30 Transformation of *Arabidopsis thaliana* was performed by vacuum infiltration (Bent et al., *Science* 265, 1856, (1994)) with minor modifications. Briefly, 500 mL cultures of transformed *Agrobacterium* harboring the pBIC20-F5H cosmid or the pGA482-35S-F5H construct were grown to stationary phase in Luria broth containing 10 mg L⁻¹ rifampicin and 50 mg L⁻¹ kanamycin. 35 Cells were harvested by centrifugation and resuspended in 1 L infiltration media containing 2.2 g MS salts (Murashige and Skoog, *Physiol. Plant.* 15, 473, (1962)), Gamborg's B5 vitamins (Gamborg et al., *Exp. Cell Res.* 50, 151, (1968)), 0.5 g MES, 50 g sucrose, 44 nM benzylaminopurine, and 200 μ L Silwet L-77 (OSI

Specialties) at pH 5.7. Bolting *Arabidopsis* plants (T_0 generation) that were 5 to 10 cm tall were inverted into the bacterial suspension and exposed to a vacuum (>500 mm of Hg) for three to five min. Infiltrated plants were returned to standard growth conditions for seed production. Transformed seedlings (T_1) were

5 identified by selection on MS medium containing 50 mg L⁻¹ kanamycin and 200 mg L⁻¹ timentin (SmithKline Beecham) and were transferred to soil.

Transformation of tobacco was accomplished using the leaf disk method of Horsch et al. (*Science* 227, 1229, (1985)).

Nitrobenzene oxidation

10 For the determination of lignin monomer composition, stem tissue was ground to a powder in liquid nitrogen and extracted with 20 mL of 0.1 M sodium phosphate buffer, pH 7.2 at 37 °C for 30 min followed by three extractions with 80% ethanol at 80 °C. The tissue was then extracted once with acetone and completely dried. Tissue was saponified by treatment with 1.0 M NaOH at 37 °C

15 for 24 hours, washed three times with water, once with 80% ethanol, once with acetone, and dried. Nitrobenzene oxidation of stem tissue samples was performed with a protocol modified from Iiyama et al. (*J. Sci. Food Agric.* 51, 481-491.

(1990)). Samples of lignocellulosic material (5 mg each) were mixed with 500 μ L of 2 M NaOH and 25 μ L of nitrobenzene. This mixture was incubated in a sealed glass tube at 160 °C for 3 h. The reaction products were cooled to room temperature and 5 μ L of a 20 mg mL⁻¹ solution of 3-ethoxy-4-hydroxybenzaldehyde in pyridine was added as an internal standard before the mixture was extracted twice with 1 mL of dichloromethane. The aqueous phase was acidified with HCl (pH 2) and extracted twice with 900 μ L of ether. The combined ether phases were dried with anhydrous sodium sulfate and the ether was evaporated in a stream of nitrogen. The dried residue was resuspended in 50 μ L of pyridine, 10 μ L of BSA (N,O-bis-(trimethylsilyl)-trifluoracetamide) was added and 1 μ L aliquots of the silylated products were analyzed using a Hewlet-Packard 5890 Series II gas chromatograph equipped with Supelco SPB I column (30 m x 0.75 mm). Lignin monomer composition was calculated from the integrated areas of the peaks representing the trimethylsilylated derivatives of vanillin, syringaldehyde, vanillic acid and syringic acid. Total nitrobenzene oxidation-susceptible guaiacyl units (vanillin and vanillic acid) and syringyl units (syringaldehyde and syringic acid) were calculated following correction for recovery efficiencies of each of the products during the extraction procedure relative to the internal standard.

EXAMPLE 1IDENTIFICATION OF THE T-DNA TAGGED ALLELE OF FAH1

A putatively T-DNA tagged *fah1* mutant was identified in a collection of T-DNA tagged lines (Feldmann et al., *Mol. Gen. Genet.* 208, 1, (1987)) (Dr. Tim Caspar, Dupont, Wilmington, DE) by screening adult plants under long wave UV light. A red fluorescent line (line 3590) was selected, and its progeny were assayed for sinapoylmalate content by TLC. The analyses indicated that line 3590 did not accumulate sinapoylmalate. Reciprocal crosses of line 3590 to a *fah1*-2 homozygote, followed by analysis of the F1 generation for sinapoylmalate content demonstrated that line 3590 was a new allele of *fah1*, and it was designated *fah1*-9.

Preliminary experiments indicated co-segregation of the kanamycin-resistant phenotype of the T-DNA tagged mutant with the *fah1* phenotype. Selfed seed from 7 kanamycin-resistant [*fah1*-9 x FAH1] F1 plants segregated 1:3 for kanamycin resistance (*kan*^{sensitive} *kan*^{resistant}) and 3:1 for sinapoylmalate deficiency (FAH1:*fah1*). From these lines, *fah1* plants gave rise to only *kan*^{resistant}, *fah1* progeny. To determine the genetic distance between the T-DNA insertion and the FAH1 locus, multiple test crosses were performed between a [*fah1*-9 x FAH1] F1 and a *fah1*-2 homozygote. The distance between the FAH1 locus and the T-DNA insertion was evaluated by determining the frequency at which FAH1/*kan*^{sensitive} progeny were recovered in the test cross F1. In the absence of crossover events, all kanamycin-resistant F1 progeny would be unable to accumulate sinapoylmalate, and would thus fluoresce red under UV light. In 682 *kan*^{resistant} F1 progeny examined, no sinapoylmalate proficient plants were identified, indicating a very tight linkage between the T-DNA insertion site and the FAH1 locus.

EXAMPLE 2PLASMID RESCUE AND cDNA CLONING OF THE *fah1* GENE

Plasmid rescue was conducted using *Eco*RI-digested DNA prepared from homozygous *fah1*-9 plants (Behringer et al., (1992), *supra*). Five µg of *Eco*RI-digested genomic DNA was incubated with 125 U T4 DNA ligase overnight at 14 °C in a final volume of 1 mL. The ligation mixture was concentrated approximately four fold by two extractions with equal volumes of 2-butanol, and was then ethanol precipitated and electroporated into competent DH5- α cells as described (Newman et al., (1994), *supra*).

DNA from rescued plasmids was double digested with *Eco*RI and *Sal*I. Plasmids generated from internal T-DNA sequences were identified by the presence of triplet bands at 3.8, 2.4 and 1.2 kb and were discarded. One plasmid (pCC1) giving rise to the expected 3.8 kb band plus a novel 5.6 kb band was

identified as putative external right border plasmid. Using a *SacII/EcoRI* fragment of pCC1 that appeared to represent *Arabidopsis* DNA, putative cDNA (pCC30) clones for F5H were identified. The putative F5H clone carried a 1.9 kb *SalI-NotI* insert, the sequence of which was determined. Blastx analysis (Altschul et al., *J. Mol. Biol.* 215, 403, (1990)) indicated that this cDNA encodes a cytochrome P450-dependent monooxygenase, consistent with earlier reports that (i) the *fahl* mutant is defective in F5H (Chapple et al., *supra*) and (ii) F5H is a cytochrome P450-dependent monooxygenase (Grand, *supra*).

Southern and Northern Blot analysis

10 To determine whether the putative F5H cDNA actually represented the gene that was disrupted in the T-DNA tagged line Southern and northern analysis was used to characterize the available *fahl* mutants using the putative F5H cDNA.

15 Figure 6 shows a Southern blot comparing hybridization of the F5H cDNA to *EcoRI*-digested genomic DNA isolated from wild type (ecotypes Columbia (Col), Landsberg *erecta* (LER), and Wassilewskija (WS)) and the nine *fahl* alleles including the T-DNA tagged *fahl-9* allele. WS is the ecotype from which the T-DNA tagged line was generated.

20 These data indicated the presence of a restriction fragment length polymorphism between the tagged line and the wild type. These data also indicates a restriction fragment length polymorphism in the *fahl-8* allele which was generated with fast neutrons, a technique reported to cause deletion mutations.

25 As shown in Figure 6 the genomic DNA of the *fahl-8* and *fahl-9* (the T-DNA tagged line) alleles is disrupted in the region corresponding to the putative F5H cDNA. These data also indicate that F5H is encoded by a single gene in *Arabidopsis* as expected considering that the mutation in the *fahl* mutant segregates as a single Mendelian gene. These data provide the first indication that the putative F5H cDNA corresponds to the gene that is disrupted in the *fahl* mutants.

30 Plant material homozygous for nine independently-derived *fahl* alleles was surveyed for the abundance of transcript corresponding to the putative F5H cDNA using Northern blot analysis. The data is shown in Figure 7.

35 As can be seen from the data, the putative F5H mRNA was represented at similar levels in leaf tissue of Columbia, Landsberg *erecta* and Wassilewskija ecotypes, and in the EMS-induced *fahl-1*, *fahl-4*, and *fahl-5*, as well as the fast neutron-induced *fahl-7*. Transcript abundance was substantially reduced in leaves from plants homozygous for the *fahl-2*, *fahl-3* and *fahl-6*, all of which were EMS-induced, the fast neutron-induced mutant *fahl-8* and in the tagged line *fahl-9*. The mRNA in *fahl-8* mutant also appears to be truncated. These data provided

strong evidence that the cDNA clone that had been identified is encoded by the FAH1 locus.

EXAMPLE 3

DEMONSTRATION OF THE IDENTITY OF THE F5H cDNA BY TRANSFORMATION OF *fahl* MUTANT PLANTS WITH WILDTYPE F5H AND RESTORATION OF SINAPOYLMALATE ACCUMULATION

In order to demonstrate the identity of the F5H gene at the functional level, the transformation-competent pBIC20 cosmid library (Meyer et al., *supra*) was screened for corresponding genomic clones using the full length F5H cDNA as a probe. A clone (pBIC20-F5H) carrying a genomic insert of 17 kb that contains 2.2 kb of sequence upstream of the putative F5H start codon and 12.5 kb of sequence downstream of the stop codon of the F5H gene (Figure 2) was transformed into the *fahl*-2 mutant by vacuum infiltration. Thirty independent infiltration experiments were performed, and 167 kanamycin-resistant seedlings, representing at least 3 transformants from each infiltration, were transferred to soil and were analyzed with respect to sinapic acid-derived secondary metabolites. Of these plants, 164 accumulated sinapoylmalate in their leaf tissue as determined by TLC (Figure 3). These complementation data indicate that the gene defective in the *fahl* mutant is present on the binary cosmid pBIC20-F5H.

To delimit the region of DNA on the pBIC20-F5H cosmid responsible for complementation of the mutant phenotype, a 2.7 kB fragment of the F5H genomic sequence was fused downstream of the cauliflower mosaic virus 35S promoter in the binary plasmid pGA482 and this construct (pGA482-35S-F5H) (Figure 2) was transformed into the *fahl*-2 mutant. The presence of sinapoylmalate in 109 out of 110 transgenic lines analyzed by TLC or by *in vivo* fluorescence under UV light indicated that the *fahl* mutant phenotype had been complemented (Figure 3). These data provide conclusive evidence that the F5H cDNA has been identified.

EXAMPLE 4

DNA SEQUENCING OF THE F5H cDNA AND GENOMIC CLONES

The F5H cDNA and a 5156 bp *Hind*III-*Xba*I fragment of the pBIC20-F5H genomic clone were both fully sequenced on both strands and the sequence of the F5H protein (SEQ ID NO.:2) was inferred from the cDNA sequence (Figure 8). The sequence of the *Arabidopsis thaliana* F5H cDNA is given in SEQ ID NO.:1. The sequence of the *Arabidopsis thaliana* F5H genomic clone is given in SEQ ID NO.:3.

EXAMPLE 5MODIFICATION OF LIGNIN MONOMER COMPOSITION IN
TRANSGENIC PLANTS OVEREXPRESSING F5HGeneration of Transgenic Plants Ectopically Expressing the F5H Gene

5 Using an adaptor-based cloning strategy, regulatory sequences 5' of the translation initiation site of the F5H gene were replaced with the strong constitutive cauliflower mosaic virus 35S promoter (Odell et al., *Nature* 313, 810-812. (1985)), as shown in Figure 2. The resulting construct carries 2719 bp of the F5H genomic sequence driven by the cauliflower mosaic virus 35S promoter
10 fused 50 bp upstream of the inferred ATG start codon. As a result, the cauliflower mosaic virus 35S promoter drives the expression of the F5H gene by using the transcription start site of the viral promoter and the termination signal present on the F5H genomic sequence. This expression cassette for ectopic expression of F5H was inserted into the T-DNA of the binary vector pGA482 (An, G. (1987),
15 *Binary Ti vectors for plant transformation and promoter analysis in: Methods in enzymology*. Wu, R. ed. Academic Press, NY 153: 292-305) and introduced into *Agrobacterium tumefaciens* by electroporation.

18 Transgenic *Arabidopsis* plants of the ecotype Columbia that were homozygous for the *fah1-2* (Chapple et al., *supra*) allele were transformed with
20 *Agrobacterium* cultures harboring the pGA482-35S-F5H construct according to the method of Bent et al. (*supra*). Transgenic plants of the T2 and T3 generation were identified by selection on media containing kanamycin and subsequently transferred to soil.

Determination of lignin monomer composition of *Arabidopsis* stem tissue

25 Total stem tissue was harvested from 4 week old plants that had been grown in soil at 22 °C under a 16 h/8 h light/dark photoperiod. Nitrobenzene oxidation analysis generated mol% syringyl values for 9 different transformant lines (Table 1) ranging from 5.06 +/- 0.17 mol% to 28.8 +/- 0.92 mol% as opposed to the wildtype control which demonstrated a value of 18.4 +/- 0.91 mol%. The
30 *fah1-2* mutant background in which the transgenic lines were generated completely lacks syringyl lignin (Table 1). The low expression of the F5H transgene in a genetic background that lacks endogenous F5H message explains how line 88 can have syringyl lignin levels that are lower than wild type.

35 In addition to *Arabidopsis*, tobacco plants were transformed in a similar fashion with the F5H gene under control of the cauliflower mosaic virus 35S promoter. T2 and T3 positive transformants were screened and analyzed for lignin modification and the data is given in Table 2. Nitrobenzene oxidation analysis of tobacco leaf midribs generated mol% syringyl values for 4 different transformant

lines (Table 2) ranging from 22.4 +/- 1.53 mol% to 40.0 +/- 1.86 mol% as opposed to the wildtype control which demonstrated a value of 14.3 +/- 1.09 mol%.

The data in Tables 1 and 2 clearly demonstrate that over-expression of the F5H gene in transgenic plants results in the modification of lignin monomer composition. The transformed plant is reasonably expected to have syringyl lignin monomer content that is from about 0 mol% to about 95 mol% as measured in whole plant tissue.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: PURDUE RESEARCH FOUNDATION
- (B) STREET: 1650 ENGINEERING ADM BLDG, ROOM 328
- (C) CITY: WEST LAFAYETTE
- (D) STATE: INDIANA
- (E) COUNTRY: UNITED STATES OF AMERICA
- (F) POSTAL CODE (ZIP): 47907-1650
- (G) TELEPHONE: 317-494-2610
- (H) TELEFAX: 317-496-1277
- (I) TELEX:

(ii) TITLE OF INVENTION: A METHOD FOR REGULATION OF
PLANT LIGNIN COMPOSITION

(iii) NUMBER OF SEQUENCES: 3

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: DISKETTE, 3.50 INCH
- (B) COMPUTER: IBM PC COMPATIBLE
- (C) OPERATING SYSTEM: WINDOWS 3.1
- (D) SOFTWARE: MICROSOFT WORD 2.0C

(v) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 60/009,119
- (B) FILING DATE: DECEMBER 22, 1995

(vii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: THOMAS Q. HENRY
- (B) REGISTRATION NO.: 28,309
- (C) REFERENCE/DOCKET NUMBER: CR-9870

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1838 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (cDNA)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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AGTCCTTCAA	GTCCAAGACA	GCGTCTTCTC	GAACCGGCCT	GCAACTATAG	CTATAAGCTA	360
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TCGTGATGAA	GTGGACAAAA	TGGTCCGGTC	GGTCTCTTGT	AACGTTGGTA	AGCCTATAAAA	540
CGTCGGGGAG	CAAATTTTG	CACTGACCCG	CAACATAACT	TACCGGGCAG	CGTTTGGGTC	600
AGCCTGCGAG	AAGGGACAAG	ACGAGTTCAT	AAGAATCTTA	CAAGAGTTCT	CTAAGCTTTT	660
TGGAGCCTTC	AACGTAGCGG	ATTCATACC	ATATTCGGG	TGGATCGATC	CGCAAGGGAT	720
AAACAAGCGG	CTCGTGAAGG	CCCGTAATGA	TCTAGACGGA	TTTATTGACG	ATATTATCGA	780
TGAACATATG	AAGAAGAAGG	AGAATCAAAA	CGCTGTGGAT	GATGGGGATG	TTGTCGATAC	840
CGATATGGTT	GATGATCTTC	TTGCTTTTA	CAGTGAAGAG	GCCAAATTAG	TCAGTGAGAC	900
AGCGGATCTT	CAAAATTCCA	TCAAACCTAC	CCGTGACAAT	ATCAAAGCAA	TCATCATGGA	960
CGTTATGTTT	GGAGGAACGG	AAACGGTAGC	CTCGGCATA	GAGTGGGCCT	TAACGGAGTT	1020
ATTACGGAGC	CCCGAGGATC	TAAAACGGGT	CCAACAAGAA	CTCGCCGAAG	TCGTTGGACT	1080
TGACAGACGA	GTTGAAGAAT	CCGACATCGA	GAAGTTGACT	TATCTCAAAT	GCACACTCAA	1140
AGAAACCCCTA	AGGATGCACC	CACCGATCCC	TCTCCTCCTC	CACGAAACCG	CGGAGGACAC	1200
TAGTATCGAC	GGTTTCTTC	TTCCCAAGAA	ATCTCGTGTG	ATGATCAACG	CGTTTGCAT	1260
AGGACGGGAC	CCAACCTCTT	GGACTGACCC	GGACACGTTT	AGACCATCGA	GGTTTTGGA	1320
ACCGGGCGTA	CCGGATTTC	AAGGGAGCAA	TTTCGAGTTT	ATACCGTTCG	GGTCGGGTCG	1380
TAGATCGTGC	CCGGGTATGC	AACTAGGGTT	ATACGCGCTT	GACTTAGCCG	TGGCTCATAT	1440
ATTACATTGC	TTCACGTGGA	AATTACCTGA	TGGGATGAAA	CCAAGTGAGC	TCGACATGAA	1500
TGATGTGTTT	GGTCTCACGG	CTCCTAAAGC	CACGCGGCTT	TTCGCCGTGC	CAACCACGCG	1560

CCTCATCTGT GCTCTTAAG TTTATGGTTC GAGTCACGTG GCAGGGGGTT TGGTATGGTG 1620
 AAAACTGAAA AGTTTGAAGT TGCCCTCATC GAGGATTGT GGATGTCATA TGTATGTATG 1680
 TGTATACACG TGTGTTCTGA TGAAAACAGA TTTGGCTCTT TGTTTGCCCT TTTTTTTTT 1740
 TTCTTTAATG GGGATTTCC TTGAATGAAA TGAAACAGTA AAAATAAGAT TTTTTCAAT 1800
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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 520 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Ser Ser Ile Ser Gln Thr Leu Ser Lys Leu Ser Asp Pro Thr
 1 5 10 15
 Thr Ser Leu Val Ile Val Val Ser Leu Phe Ile Phe Ile Ser Phe Ile
 20 25 30
 Thr Arg Arg Arg Arg Pro Pro Tyr Pro Pro Gly Pro Arg Gly Trp Pro
 35 40 45
 Ile Ile Gly Asn Met Leu Met Met Asp Gln Leu Thr His Arg Gly Leu
 50 55 60
 Ala Asn Leu Ala Lys Lys Tyr Gly Gly Leu Cys His Leu Arg Met Gly
 65 70 75 80
 Phe Leu His Met Tyr Ala Val Ser Ser Pro Glu Val Ala Arg Gln Val
 85 90 95
 Leu Gln Val Gln Asp Ser Val Phe Ser Asn Arg Pro Ala Thr Ile Ala
 100 105 110
 Ile Ser Tyr Leu Thr Tyr Asp Arg Ala Asp Met Ala Phe Ala His Tyr
 115 120 125
 Gly Pro Phe Trp Arg Gln Met Arg Lys Val Cys Val Met Lys Val Phe
 130 135 140
 Ser Arg Lys Arg Ala Glu Ser Trp Ala Ser Val Arg Asp Glu Val Asp
 145 150 155 160
 Lys Met Val Arg Ser Val Ser Cys Asn Val Gly Lys Pro Ile Asn Val
 165 170 175
 Gly Glu Gln Ile Phe Ala Leu Thr Arg Asn Ile Thr Tyr Arg Ala Ala
 180 185 190
 Phe Gly Ser Ala Cys Glu Lys Gly Gln Asp Glu Phe Ile Arg Ile Leu
 195 200 205
 Gln Glu Phe Ser Lys Leu Phe Gly Ala Phe Asn Val Ala Asp Phe Ile
 210 215 220

Pro Tyr Phe Gly Trp Ile Asp Pro Gln Gly Ile Asn Lys Arg Leu Val
 225 230 235 240
 Lys Ala Arg Asn Asp Leu Asp Gly Phe Ile Asp Asp Ile Ile Asp Glu
 245 250 255
 His Met Lys Lys Lys Glu Asn Gln Asn Ala Val Asp Asp Gly Asp Val
 260 265 270
 Val Asp Thr Asp Met Val Asp Asp Leu Leu Ala Phe Tyr Ser Glu Glu
 275 280 285
 Ala Lys Leu Val Ser Glu Thr Ala Asp Leu Gln Asn Ser Ile Lys Leu
 290 295 300
 Thr Arg Asp Asn Ile Lys Ala Ile Ile Met Asp Val Met Phe Gly Gly
 305 310 315 320
 Thr Glu Thr Val Ala Ser Ala Ile Glu Trp Ala Leu Thr Glu Leu Leu
 325 330 335
 Arg Ser Pro Glu Asp Leu Lys Arg Val Gln Gln Glu Leu Ala Glu Val
 340 345 350
 Val Gly Leu Asp Arg Arg Val Glu Glu Ser Asp Ile Glu Lys Leu Thr
 355 360 365
 Tyr Leu Lys Cys Thr Leu Lys Glu Thr Leu Arg Met His Pro Pro Ile
 370 375 380
 Pro Leu Leu Leu His Glu Thr Ala Glu Asp Thr Ser Ile Asp Gly Phe
 385 390 395 400
 Phe Ile Pro Lys Lys Ser Arg Val Met Ile Asn Ala Phe Ala Ile Gly
 405 410 415
 Arg Asp Pro Thr Ser Trp Thr Asp Pro Asp Thr Phe Arg Pro Ser Arg
 420 425 430
 Phe Leu Glu Pro Gly Val Pro Asp Phe Lys Gly Ser Asn Phe Glu Phe
 435 440 445
 Ile Pro Phe Gly Ser Gly Arg Arg Ser Cys Pro Gly Met Gln Leu Gly
 450 455 460
 Leu Tyr Ala Leu Asp Leu Ala Val Ala His Ile Leu His Cys Phe Thr
 465 470 475 480
 Trp Lys Leu Pro Asp Gly Met Lys Pro Ser Glu Leu Asp Met Asn Asp
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 Val Phe Gly Leu Thr Ala Pro Lys Ala Thr Arg Leu Phe Ala Val Pro
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(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5156 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AAGCTTATGT	ATTCCTTAT	AACCATTTA	TTCTGTATAT	AGGGGGACAG	AAACATAATA	60
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GTCACTAAAT	AGTTTAAAAA	GACACGAAGT	TGGTAAGAAC	AGGCATATAT	TATTGAGATT	240
AATTAGGAAT	GCTTATGTTA	ATCTGATTG	ACTAATTAGA	AACGACGATA	CTATGAGCTC	300
ATAGATGGTC	CCACGACCCA	CTCTCCCATT	TGATCAATAT	TCAACTGAGC	AATGAAACTA	360
ATTAAAAACG	TGGTTAGATT	AAAAAAATAA	ATTGTGCAGG	TAGCGGATAT	ATAATACTAG	420
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AATAGTTTT	TTGCTTCAAA	AATATCACAA	ATTTTTGTAT	GAAATATTTC	TTAACGAAA	540
ATAAAATTAAA	AAAAATTAA	AATTTATATT	TGGAGTTCTA	TTTTAATT	AGAGTTTTA	600
TTGTTACAC	ATTTTTGAA	TTATTCTAAT	ATTAATTGT	GATATTATTA	CAAAAAGTAA	660
AAATATGATA	TTTTAGAATA	CTATTATCGA	TATTTGATAT	TATTGACCTT	AGCTTTGTT	720
GGGTGGAGAC	ATGTGATTAT	CTTATTACCT	TTTATTCCA	TGAAACTACA	GAGTCGCCA	780
GGTACCATAC	ATGCACACAC	CCTCGTGAAG	CCGTGACTTA	ATATGATCTA	GAACCTAAAT	840
AGTACTACTA	ATTGTGTCAT	TTGAACCTTC	TCCTATGTCG	GTTTCACTTC	ATGTATCGCA	900
GAACAGGTGG	AATACAGTGT	CCTTGAGTTT	CACCCAAATC	GGTCCAATT	TGTGATATAT	960
ATTGCGATAC	AGACATACAG	CCTACAGAGT	TTTGTCTTAG	CCCACTGGTT	GGCAAACGAA	1020
ATTGTCTTA	TTTTTTATG	TTTGTTGTC	AATGTGTCTT	TGTTTTAAC	TAGATTGAGG	1080
TTTAATTAA	ATACATTGT	TAGTTTACAG	ATTATGCACT	GTAATCTGAT	AATGTAAGTT	1140
GAACTGCGTT	GGTCAAAGTC	TTGTGTAACG	CACTGTATCT	AAATTGTGAG	TAACGACAAA	1200
ATAAAATTAAA	TTAAAGGACC	TTCAAGTATT	ATTAGTATCT	CTGTCTAAGA	TGCACAGGTA	1260
TTCAGTAATA	GTAATAAAATA	ATTACTGTA	TAATTAATAT	CTAATTAGTA	AACCTTGTGT	1320
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ACGAAAAAAA	GAACCAAAAGA	CTACCTGAAA	AGTCATGCAC	AACGTTCATC	1440	
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AAAAAAAAT	TTTTTTTAG	TTATTCACC	TTTTTCTTTT	GTTCTGGTTG	TATGGTTGCC	4860
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CTAAGGTTTT	TATTAGTTT	ATTTTCAGTT	TACTGAGTAC	TATTTACTTT	TTTATTTTT	5040
GCAAATAAAAT	GTATTTTATC	ATATTTATGT	TTTTTGTAT	AAACTCCAAA	CATACAGGTT	5100
TCATTACCTA	AAAAAAAGACA	GAGTGGTTTC	GTAAATTTG	TTTCATTAAT	CTCGAG	5156

WHAT IS CLAIMED IS:

1. An isolated nucleic-acid fragment encoding an active plant F5H enzyme having an amino acid sequence encoded by a mature functional protein which corresponds to SEQ ID NO.:2 and wherein the amino acid sequence encompasses amino acid substitutions, additions and deletions that do not alter the function of the active plant F5H enzyme.
- 5 2. An isolated nucleic-acid fragment selected from the group consisting of nucleic acid fragments corresponding to SEQ ID NO.:1 and SEQ ID NO.:3.
- 10 3. A chimeric gene causing altered guaiacyl:syringyl lignin monomer ratios in a plant cell transformed with the chimeric gene, the chimeric gene comprising the nucleic acid fragment of Claims 1 or 2 operably linked in either sense or antisense orientation to at least one suitable regulatory sequence.
- 15 4. The chimeric gene of Claim 3 wherein the nucleic acid fragment is operably linked in the sense orientation to at least one suitable regulatory sequence.
5. The chimeric gene of Claims 3 wherein the at least one regulatory sequence comprises a promoter selected from the group consisting of cauliflower mosaic virus 35S promoter, the promoter for the phenylalanine ammonia lyase gene, the promoter for the *p*-coumaroyl CoA ligase gene, and endogenous plant promoters capable of controlling expression of plant F5H genes.
- 20 6. A transformed plant having altered guaiacyl:syringyl lignin monomer ratios relative to the ratios of an untransformed plant and comprising a suitable host plant and the chimeric gene of Claims 3.
7. The transformed plant of Claim 6 wherein the syringyl lignin monomer content is from about 0 mol% to about 95 mol% as measured in whole plant tissue.
- 25 8. The transformed plant of Claim 7 wherein the suitable host plant is selected from the group consisting of alfalfa (*Medicago* sp.), rice (*Oryza* sp.), maize (*Zea mays*), oil seed rape (*Brassica* sp.), forage grasses, *Arabidopsis* sp., tobacco (*Nicotiana* sp.) and tree crops such as eucalyptus (*Eucalyptus* sp.), pine (*Pinus* sp.), spruce (*Picea* sp.) and poplar (*Populus* sp.).
- 30 9. A method of altering the activity of F5H enzyme in a plant, comprising:
 - (i) transforming a cell, tissue or organ from a suitable host plant with the chimeric gene of Claim 3 wherein the chimeric gene is expressed;
 - (ii) selecting transformed cells, cell callus, somatic embryos, or seeds which contain the chimeric gene;
 - 35 (iii) regenerating whole plants from the transformed cells, cell callus, somatic embryos, or seeds selected in step (ii);
 - (iv) selecting whole plants regenerated in step (iii) which have a phenotype characterized by (1) an ability of the whole plant to accumulate

compounds derived from sinapic acid or (2) an altered syringyl lignin monomer content relative to an untransformed host plant.

10. A method of altering the content or composition of lignin in a plant, comprising stably incorporating the chimeric gene of Claim 3 into the genome of the host plant by transformation means whereby the incorporated chimeric gene expresses F5H enzyme and whereby guaiacyl:syringyl lignin monomer ratios are altered from those of the untransformed host plant.

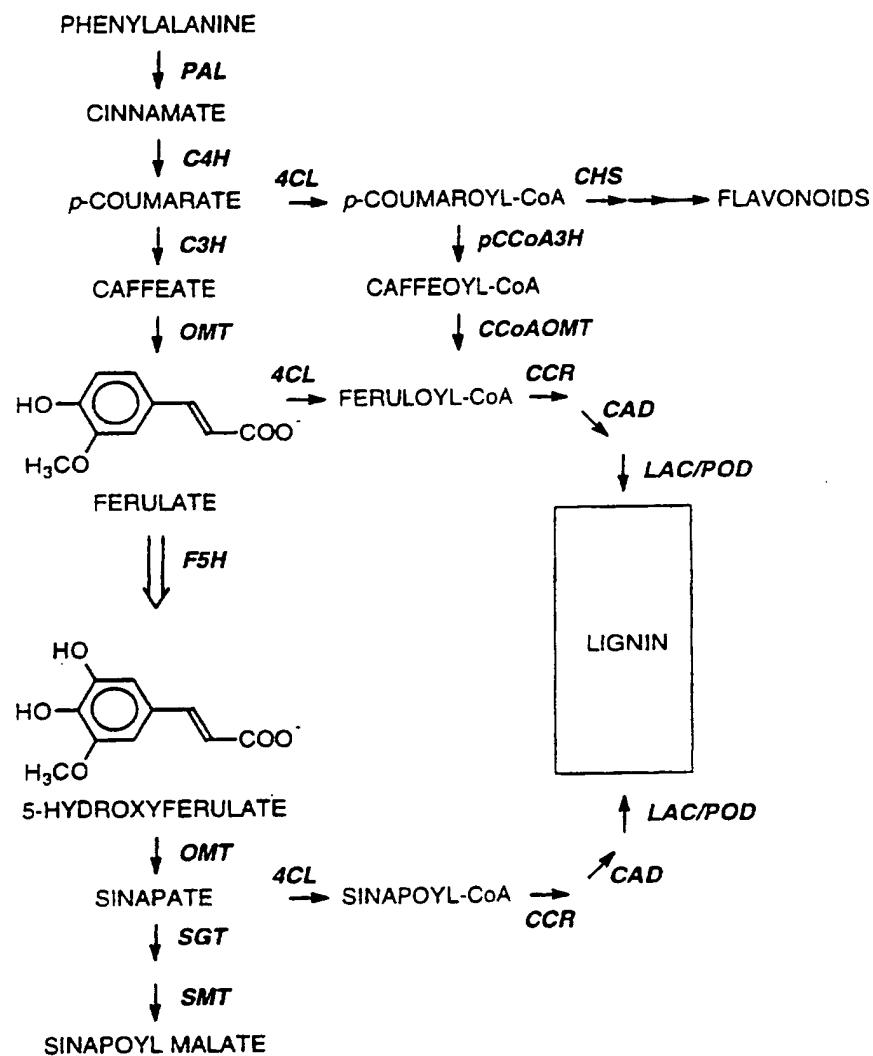


Figure 1

WO 97/23599

PCT/US96/20094

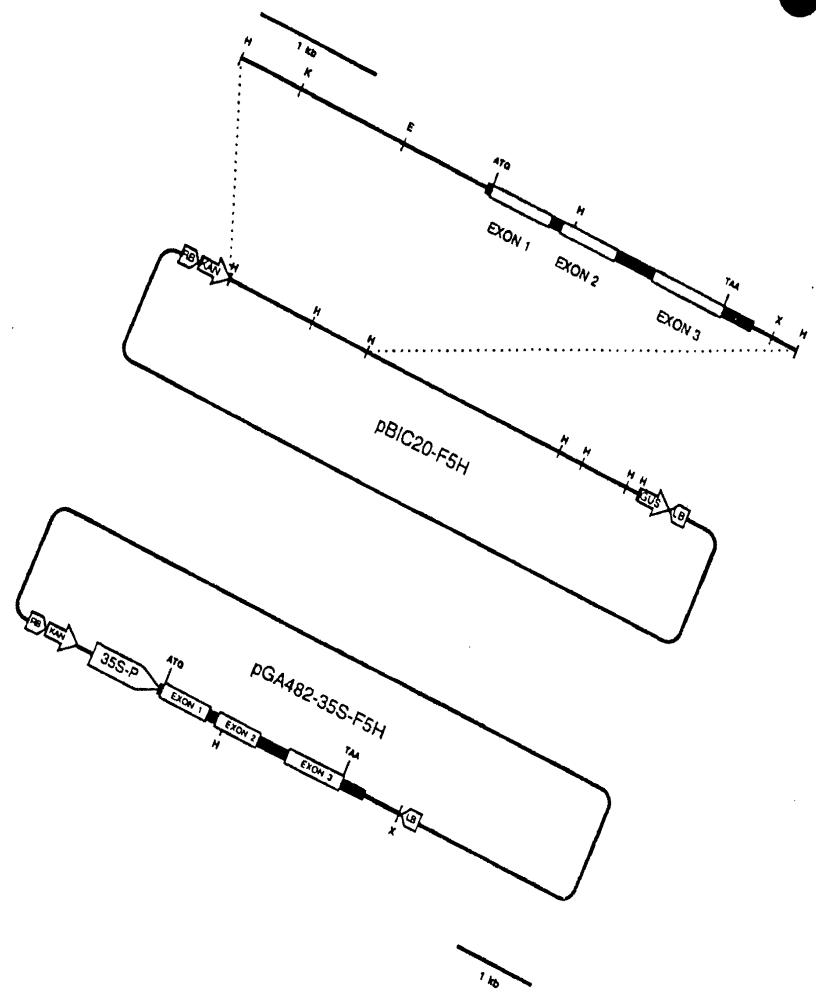


Figure 2
2/8

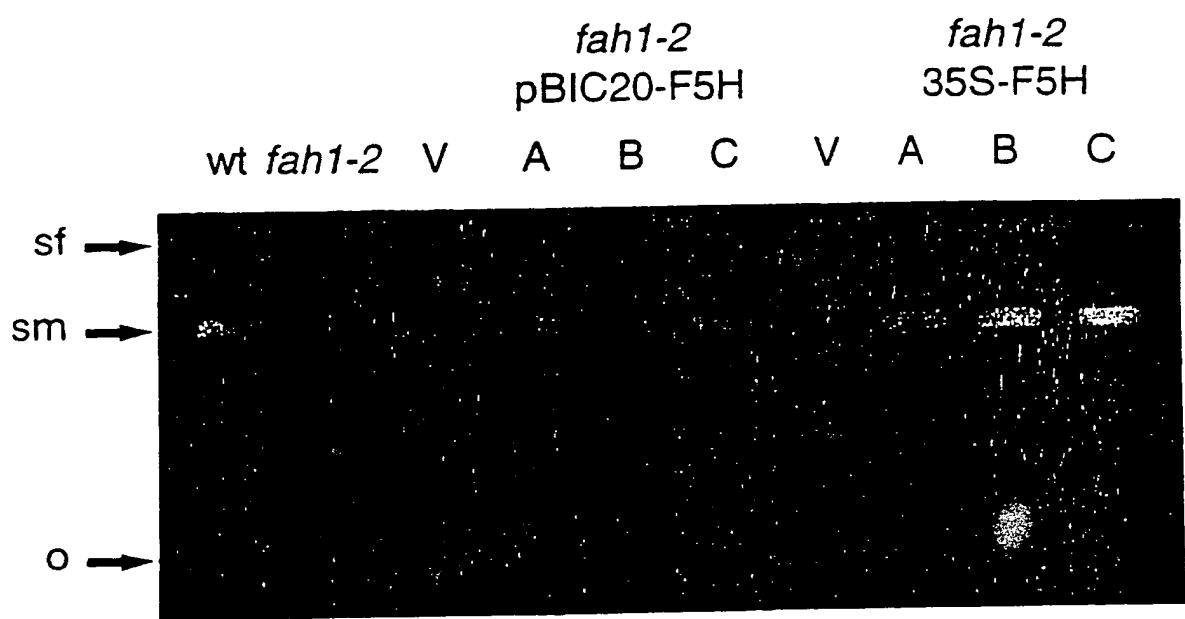
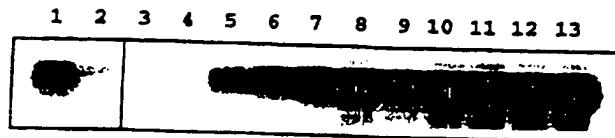


Figure 3

**24 hour exposure**

1. wild type
2. *fah1-2*

2 hour exposure

3. wild type
4. *fah1-2*
5. line 88
6. line 172
7. line 170
8. line 122
9. line 128
10. line 107
11. line 180
12. line 117
13. line 108

Figure 4

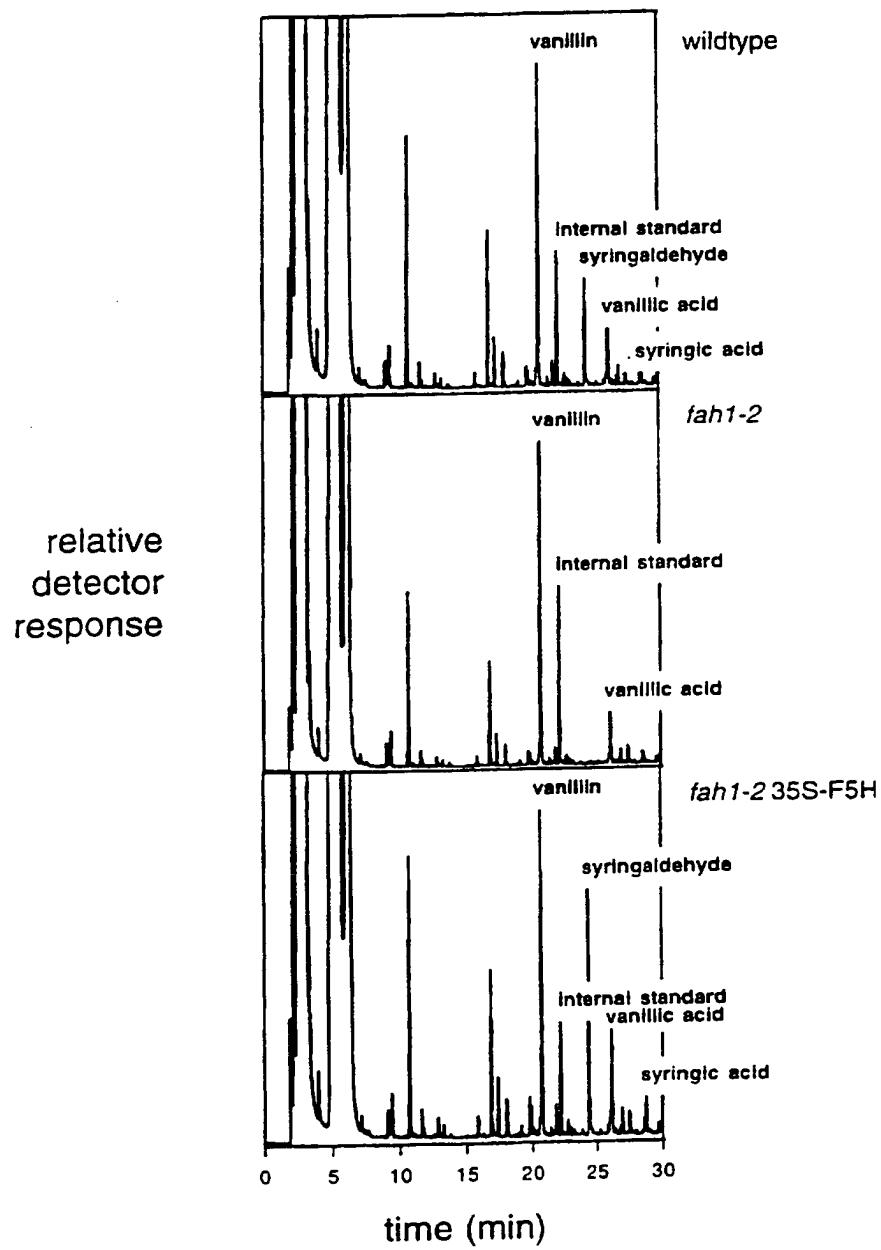


Figure 5

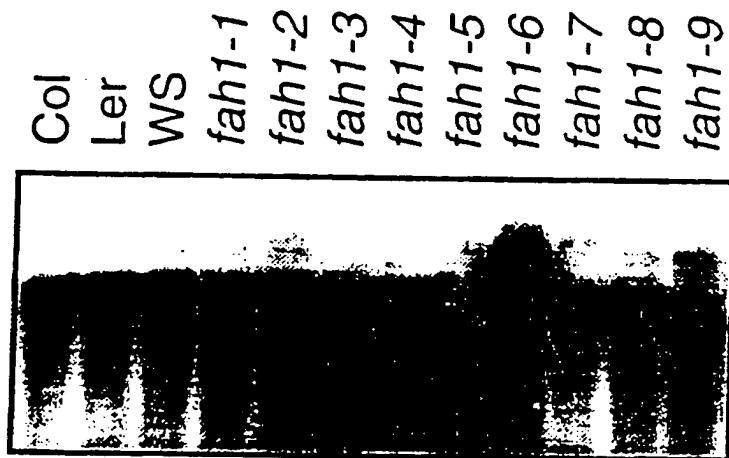


Figure 6

Col	Ler	WS	<i>fah1-1</i>	<i>fah1-2</i>	<i>fah1-3</i>	<i>fah1-4</i>	<i>fah1-5</i>	<i>fah1-6</i>	<i>fah1-7</i>	<i>fah1-8</i>	<i>fah1-9</i>

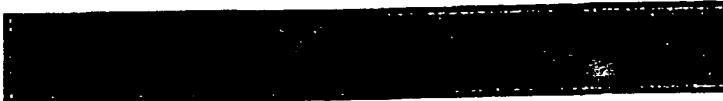


Figure 7



Figure 8





INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 6: C12N 15/29, 15/53, 9/02, 15/82, A01H 1/00, 3/00		A3	(11) International Publication Number: WO 97/23599 (43) International Publication Date: 3 July 1997 (03.07.97)
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(54) Title: A METHOD FOR REGULATION OF PLANT LIGNIN COMPOSITION

(57) Abstract

A method is disclosed for the regulation of lignin composition in plant tissue. Plants are transformed with a gene encoding an active F5H gene. The expression of the F5H gene results in increased levels of syringyl monomer providing a lignin composition more easily degraded with chemicals and enzymes.

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P, X	PROC. NATL. ACAD. SCI. USA, vol. 93, no. 14, July 1996, pages 6869-6874, XP002036466 MEYER, K. ET AL.: "Ferulate-5-hydroxylase from <i>Arabidopsis thaliana</i> defines a new family of cytochrome P450-dependent monooxygenases" see the whole document ---	1
A	PLANT PHYSIOL., vol. 108, 1995, pages 875-876, XP002036467 CHAPPLE, C.C.S.: "A cDNA encoding a novel cytochrome P450-dependent monooxygenase from <i>Arabidopsis thaliana</i> " see the whole document ---	1-5 -/-

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